

Table S1. Amino acid identity of Sphingomonadaceae ATP synthase subunit beta, Related to STAR Methods.

blastp

Iteration: 0

Query: tr|A0A0H3FY43|A0A0H3FY43_ZYMMA ATP synthase subunit beta OS=Zymomonas mobilis subsp. mobilis (strain ATCC 10988 / DSM 424 / LMG 404 / NCIMB 8938 / NRRL B-806 / ZM1) OX=555217 GN=atpD PE=3 SV=1

RID: BDU04B4M014

Database: nr

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens, q. start, q. end, s. start, s. end, evalue, bit score, % positives

query acc.ver	subject acc.ver	% identity	alignment length	mismatches	gap opens	q. start	q. end	s. start	s. end	evalue	bit score	% positives
tr A0A0H3FY43 A0A0H3FY43_ZYMMA	WP_014500718.1	100.000	484	0	0	1	484	1	484	0.0	977	100.00
tr A0A0H3FY43 A0A0H3FY43_ZYMMA	WP_011240186.1	99.793	484	1	0	1	484	1	484	0.0	974	99.79
tr A0A0H3FY43 A0A0H3FY43_ZYMMA	WP_012817426.1	99.587	484	2	0	1	484	1	484	0.0	972	99.79
tr A0A0H3FY43 A0A0H3FY43_ZYMMA	WP_014848899.1	98.760	484	6	0	1	484	1	484	0.0	965	99.17
tr A0A0H3FY43 A0A0H3FY43_ZYMMA	AEI37830.1	95.455	484	22	0	1	484	1	484	0.0	941	98.55
tr A0A0H3FY43 A0A0H3FY43_ZYMMA	WP_129791146.1	83.402	482	80	0	2	483	13	494	0.0	822	91.08
tr A0A0H3FY43 A0A0H3FY43_ZYMMA	WP_109269810.1	82.136	487	84	1	1	484	1	487	0.0	821	90.97
tr A0A0H3FY43 A0A0H3FY43_ZYMMA	WP_008600151.1	82.231	484	86	0	1	484	1	484	0.0	818	91.12
tr A0A0H3FY43 A0A0H3FY43_ZYMMA	WP_130001901.1	82.121	481	86	0	3	483	10	490	0.0	815	91.27
tr A0A0H3FY43 A0A0H3FY43_ZYMMA	WP_088711066.1	81.520	487	87	1	1	484	1	487	0.0	814	91.38
tr A0A0H3FY43 A0A0H3FY43_ZYMMA	WP_086616854.1	82.025	484	86	1	1	483	1	484	0.0	814	90.50
tr A0A0H3FY43 A0A0H3FY43_ZYMMA	WP_114686287.1	82.158	482	86	0	2	483	11	492	0.0	813	90.04
tr A0A0H3FY43 A0A0H3FY43_ZYMMA	WP_118864930.1	81.031	485	90	1	1	483	1	485	0.0	813	90.52
tr A0A0H3FY43 A0A0H3FY43_ZYMMA	WP_095011651.1	82.062	485	85	1	1	483	1	485	0.0	813	90.52
tr A0A0H3FY43 A0A0H3FY43_ZYMMA	WP_119513812.1	81.856	485	86	1	1	483	1	485	0.0	813	90.52
tr A0A0H3FY43 A0A0H3FY43_ZYMMA	WP_119591632.1	81.856	485	86	1	1	483	1	485	0.0	812	90.31
tr A0A0H3FY43 A0A0H3FY43_ZYMMA	WP_046902917.1	81.443	485	88	1	1	483	1	485	0.0	812	90.10
tr A0A0H3FY43 A0A0H3FY43_ZYMMA	WP_129523148.1	81.649	485	87	1	1	483	1	485	0.0	812	90.52
tr A0A0H3FY43 A0A0H3FY43_ZYMMA	WP_067678508.1	81.649	485	87	1	1	483	1	485	0.0	811	90.52
tr A0A0H3FY43 A0A0H3FY43_ZYMMA	WP_022687812.1	82.353	476	84	0	8	483	18	493	0.0	811	90.55
tr A0A0H3FY43 A0A0H3FY43_ZYMMA	WP_019831984.1	81.781	483	88	0	1	483	1	483	0.0	811	90.27
tr A0A0H3FY43 A0A0H3FY43_ZYMMA	WP_128893080.1	81.649	485	87	1	1	483	1	485	0.0	810	90.52
tr A0A0H3FY43 A0A0H3FY43_ZYMMA	WP_061925225.1	81.649	485	87	1	1	483	1	485	0.0	810	90.52
tr A0A0H3FY43 A0A0H3FY43_ZYMMA	WP_085219113.1	81.314	487	87	1	1	483	1	487	0.0	810	89.94
tr A0A0H3FY43 A0A0H3FY43_ZYMMA	WP_050600269.1	81.649	485	87	1	1	483	1	485	0.0	810	90.52
tr A0A0H3FY43 A0A0H3FY43_ZYMMA	WP_022676816.1	81.573	483	89	0	1	483	1	483	0.0	810	89.86
tr A0A0H3FY43 A0A0H3FY43_ZYMMA	WP_120076613.1	81.649	485	87	1	1	483	1	485	0.0	810	90.52

Protein sequence identity search was conducted using blastp at https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastp&PAGE_TYPE=BlastSearch&LINK_LC=blasthome on April 2019. Only amino acid identity higher than 80% and bit score higher than 809 are shown. *Sphingomonas* spp. are highlighted in green.

Table S2. Amino acid identity of Sphingomonadaceae T4SS, Related to STAR Methods.

blastp
Iteration: 0
Query: tr|A0A1S1HB39|A0A1S1HB39_9SPHN Type IV secretion system protein PtlG OS=Sphingomonas haloaromaticamans OX=653954 GN=ptlG PE=4 SV=1

>tr|A0A1H6TMC2|A0A1H6TMC2_9SPHN Type IV secretion system protein VirB10 OS=Sphingomonas sp. OV641 OX=1881068 GN=SAMN05428950_101288 PE=4 SV=1
>tr|A0A430BGM3|A0A430BGM3_SPHYA Conjugal transfer protein TraI OS=Sphingobium yanoikuyae OX=13690 GN=DAH51_23375 PE=4 SV=1
>tr|A0A430G9L8|A0A430G9L8_9SPHN Conjugal transfer protein TraI OS=Sphingomonas koreensis OX=93064 GN=DAH66_01830 PE=4 SV=1
>tr|A0A1E3M0S3|A0A1E3M0S3_9SPHN Conjugal transfer protein TraI OS=Sphingomonas turrisvirgatae OX=1888892 GN=BFL28_09575 PE=4 SV=1
>tr|A0A1L6J612|A0A1L6J612_9SPHN Conjugal transfer protein TraI OS=Sphingomonas koreensis OX=93064 GN=BRX40_01970 PE=4 SV=1
>tr|M4S658|M4S658_9SPHN Conjugation TrbI family protein OS=Sphingomonas sp. MM-1 OX=745310 GN=G432_13550 PE=4 SV=1
>tr|A0A126RN13|A0A126RN13_9SPHN Conjugation TrbI family protein OS=Sphingobium sp. TKS OX=1315974 GN=K426_04890 PE=4 SV=1
>tr|J2WSP3|J2WSP3_9SPHN Type IV secretory pathway, VirB10 component OS=Sphingobium sp. AP49 OX=1144307 GN=PMI04_01039 PE=4 SV=1
>tr|A0A197C4R8|A0A197C4R8_9SPHN Conjugal transfer protein TraI OS=Sphingobium sp. 20006FA OX=2056888 GN=A8O16_01555 PE=4 SV=1
>tr|A0A270BKT2|A0A270BKT2_9SPHN Conjugal transfer protein TraI OS=Sphingopyxis sp. GW247-27LB OX=2012632 GN=CD928_02100 PE=4 SV=1
>tr|A0A0W1DQY5|A0A0W1DQY5_9SPHN Conjugal transfer protein TraI OS=Sphingopyxis sp. H050 OX=1759072 GN=ATE67_09595 PE=4 SV=1
>tr|U2YNH9|U2YNH9_9SPHN Conjugal transfer protein TrbI OS=Novosphingobium tardaugens NBRC 16725 OX=1219035 GN=trbI PE=4 SV=1
>tr|A0A222WZ34|A0A222WZ34_9SPHN Conjugal transfer protein TraI OS=Blastomonas fulva OX=1550728 GN=B5J99_10620 PE=4 SV=1
>tr|A0A196M7L9|A0A196M7L9_9SPHN Conjugal transfer protein TraI OS=Sphingobium sp. TCM1 OX=453246 GN=A7Q26_10770 PE=4 SV=1
>tr|A0A2A4FVN8|A0A2A4FVN8_9SPHN Conjugal transfer protein TraI OS=Rhizorhabdus dicambivorans OX=1850238 GN=COO09_13625 PE=4 SV=1
>tr|A0A1L3ZXQ0|A0A1L3ZXQ0_9SPHN Conjugal transfer protein TraI OS=Sphingomonas sp. JJ-A5 OX=1921510 GN=BSL82_14830 PE=4 SV=1
>tr|A0A1H9KJY7|A0A1H9KJY7_9SPHN Type IV secretion system protein VirB10 OS=Sphingobium sp. YR768 OX=1884365 GN=SAMN05518866_10437 PE=4 SV=1
>tr|A0A1X9UB07|A0A1X9UB07_SPHSD Conjugal transfer protein TraI OS=Sphingomonas wittichii (strain DC-6 / KACC 16600) OX=1283312 GN=HY78_05755 PE=4 SV=1
>tr|A0A2M8QSB8|A0A2M8QSB8_9SPHN Conjugal transfer protein TraI OS=Sphingobium sp. LB126 OX=1983755 GN=CAF53_09655 PE=4 SV=1
>tr|A0A292ZB30|A0A292ZB30_SPHSA Conjugative transfer protein TrbI OS=Sphingobium fuliginis (strain ATCC 27551) OX=336203 GN=SFOMI_0572 PE=4 SV=1
>tr|A5VCN0|A5VCN0_SPHWW Conjugation TrbI family protein OS=Sphingomonas wittichii (strain RW1 / DSM 6014 / JCM 10273) OX=392499 GN=Swit_3700 PE=4 SV=1
>tr|A0A219B829|A0A219B829_9SPHN Conjugal transfer protein TraI OS=Pacificimonas flava OX=1234595 GN=B5C34_10845 PE=4 SV=1
>tr|A0A2E8ZE70|A0A2E8ZE70_9SPHN Conjugal transfer protein TraI OS=Sphingobium sp. OX=1912891 GN=CMN60_13460 PE=4 SV=1
>tr|Q1NCZ8|Q1NCZ8_SPHSS Conjugation TrbI-like protein OS=Sphingomonas sp. (strain SKA58) OX=314266 GN=SKA58_16228 PE=4 SV=1
>tr|A0A0P0D4I1|A0A0P0D4I1_SPHMC Conjugal transfer protein TraI OS=Sphingopyxis macrogoltabida OX=33050 GN=LH19_06020 PE=4 SV=1
>tr|A0A0J9CZB4|A0A0J9CZB4_SPHYA Conjugal transfer protein TraI OS=Sphingobium yanoikuyae OX=13690 GN=BV87_12045 PE=4 SV=1

>tr|A0A1E4MEB9|A0A1E4MEB9_9SPHN Conjugal transfer protein TraI OS=Novosphingobium sp. SCN 66-18 OX=1660121 GN=ABT11_11220 PE=4 SV=1

>tr|A0A2D4Y8H9|A0A2D4Y8H9_9SPHN Conjugal transfer protein TraI OS=Sphingomonadaceae bacterium OX=1930536 GN=CMN67_16185 PE=4 SV=1

>tr|A0A2E9CJ58|A0A2E9CJ58_9SPHN Conjugal transfer protein TraI OS=Sphingobium sp. OX=1912891 GN=CMN64_05055 PE=4 SV=1

>tr|A0A2D6H2L4|A0A2D6H2L4_9SPHN Conjugal transfer protein TraI OS=Blastomonas sp. OX=1909299 GN=CL680_08160 PE=4 SV=1

>tr|A0A1G3KSH1|A0A1G3KSH1_9SPHN Conjugal transfer protein TraI OS=Sphingopyxis sp. RIFCSPHIGHO2_12_FULL_65_19 OX=1802172 GN=A3E77_17870 PE=4 SV=1

>tr|A0A031JY56|A0A031JY56_9SPHN Conjugal transfer protein TrbI OS=Novosphingobium resinovorum OX=158500 GN=BV97_02492 PE=4 SV=1

>tr|A0A0M4CXM5|A0A0M4CXM5_SPHS1 Conjugal transfer protein TraI OS=Sphingopyxis sp. (strain 113P3) OX=292913 GN=LH20_20550 PE=4 SV=1

>tr|A0A031IYP9|A0A031IYP9_SPHPI Conjugal transfer protein TrbI OS=Sphingomonas paucimobilis OX=13689 GN=BV96_04506 PE=4 SV=1

>tr|T0H7F9|T0H7F9_9SPHN Conjugal transfer protein TraI OS=Sphingobium lactosutens DS20 OX=1331060 GN=RLDS_21115 PE=4 SV=1

>tr|A0A2W5CEU1|A0A2W5CEU1_9SPHN Conjugal transfer protein TraI OS=Sphingomonas hengshuiensis OX=1609977 GN=DI607_07950 PE=4 SV=1

>tr|W1L0D5|W1L0D5_9SPHN Conjugal transfer protein TraI OS=Sphingobium chinhatense IP26 OX=1346790 GN=M527_11465 PE=4 SV=1

>tr|T0G9E8|T0G9E8_9SPHN Conjugal transfer protein TraI OS=Sphingobium sp. HDIP04 OX=428994 GN=L286_17785 PE=4 SV=1

>tr|A0A081T1C5|A0A081T1C5_9SPHN Conjugal transfer protein TraI OS=Sphingobium lucknowense F2 OX=1450518 GN=AL00_12660 PE=4 SV=1

>tr|A0A0S3EW84|A0A0S3EW84_9SPHN Conjugal transfer protein TraI OS=Sphingobium baderi OX=1332080 GN=ATN00_04565 PE=4 SV=1

>tr|A0A258EB63|A0A258EB63_9SPHN Conjugal transfer protein TraI OS=Sphingomonadales bacterium 32-67-7 OX=1970595 GN=B7Z07_02335 PE=4 SV=1

>tr|A0A1M3P942|A0A1M3P942_9SPHN Conjugal transfer protein TraI OS=Sphingobium sp. 66-54 OX=1895845 GN=BGP16_04495 PE=4 SV=1

>tr|G2ILW1|G2ILW1_SPHSK Conjugal transfer protein TrbI OS=Sphingobium sp. (strain NBRC 103272 / SYK-6) OX=627192 GN=SLG_30290 PE=4 SV=1

>tr|W9C133|W9C133_9SPHN Conjugal transfer protein TraI OS=Blastomonas sp. CACIA14H2 OX=1419876 GN=Q27BB25_06695 PE=4 SV=1

>tr|A0A1M3PTW1|A0A1M3PTW1_9SPHN Conjugal transfer protein TraI OS=Sphingobium sp. 66-54 OX=1895845 GN=BGP16_09665 PE=4 SV=1

>tr|A0A411LE81|A0A411LE81_SPHPI TrbI/VirB10 family protein OS=Sphingomonas paucimobilis OX=13689 GN=DRN02_000205 PE=4 SV=1

>tr|A0A2D6H4P8|A0A2D6H4P8_9SPHN Conjugal transfer protein TraI OS=Blastomonas sp. OX=1909299 GN=CL680_11880 PE=4 SV=1

>tr|A0A3N9RIJ6|A0A3N9RIJ6_9SPHN TrbI/VirB10 family protein OS=Novosphingobium sp. LASN5T OX=2491021 GN=EH199_21120 PE=4 SV=1

>tr|A0A1L6J933|A0A1L6J933_9SPHN Conjugal transfer protein TraI OS=Sphingomonas koreensis OX=93064 GN=BRX40_06140 PE=4 SV=1

>tr|A0A258GR23|A0A258GR23_9SPHN Conjugal transfer protein TraI OS=Sphingomonadales bacterium 32-64-22 OX=1970593 GN=B7Y87_01650 PE=4 SV=1

>tr|A0A1S1H9E4|A0A1S1H9E4_9SPHN Type IV secretion system protein virB10 OS=Sphingomonas haloaromaticamans OX=653954 GN=BHE75_00669 PE=4 SV=1

>tr|A0A1X9YCB3|A0A1X9YCB3_9SPHN Conjugal transfer protein TraI OS=Sphingomonas sp. KC8 OX=1030157 GN=KC8_03770 PE=4 SV=1

>tr|A0A2W6X5J5|A0A2W6X5J5_SPHSX Conjugal transfer protein TraI OS=Sphingomonas sp. OX=28214 GN=DI568_15805 PE=4 SV=1

>tr|A0A0S3EYY9|A0A0S3EYY9_9SPHN Conjugal transfer protein TraI OS=Sphingobium baderi OX=1332080 GN=ATN00_10410 PE=4 SV=1

>tr|A0A1G4TDF0|A0A1G4TDF0_9SPHN Type IV secretion system protein VirB10 OS=Sphingobium faniae OX=570446 GN=SAMN02927924_02887 PE=4 SV=1

>tr|A0A1E1EYG6|A0A1E1EYG6_9SPHN Conjugation TrbI family protein OS=Sphingobium cloacae OX=120107 GN=SCLO_1002680 PE=4 SV=1

>tr|T0H600|T0H600_9SPHN Conjugal transfer protein TraI OS=Sphingobium lactosutens DS20 OX=1331060
 GN=RLDS_21685 PE=4 SV=1
 >tr|A0A258H767|A0A258H767_9SPHN Conjugal transfer protein TraI OS=Sphingomonas sp. 32-66-10
 OX=1970437 GN=B7Y97_00950 PE=4 SV=1
 >tr|A0A430C8Z7|A0A430C8Z7_SPHYA Conjugal transfer protein TraI OS=Sphingobium yanoikuyae
 OX=13690 GN=DAH51_01980 PE=4 SV=1
 >tr|W1RXU1|W1RXU1_9SPHN Conjugal transfer protein TraI OS=Sphingobium sp. C100 OX=1207055
 GN=C100_18840 PE=4 SV=1
 >tr|A0A1G4R086|A0A1G4R086_9SPHN Type IV secretion system protein VirB10 OS=Sphingobium faniae
 OX=570446 GN=SAMN02927924_00991 PE=4 SV=1
 >tr|A0A397NI95|A0A397NI95_9SPHN Type IV secretion system protein VirB10 OS=Hephaestia caeni
 OX=645617 GN=DFR49_3140 PE=4 SV=1
 >tr|A0A2W5A0W7|A0A2W5A0W7_9SPHN Conjugal transfer protein TraI OS=Sphingomonas sanxanigenens
 OX=397260 GN=DI623_15095 PE=4 SV=1
 >tr|A0A2W6VAP1|A0A2W6VAP1_SPHSX Conjugal transfer protein TraI OS=Sphingomonas sp. OX=28214
 GN=DI568_14790 PE=4 SV=1
 >tr|A0A1Y2QE25|A0A1Y2QE25_9SPHN Conjugal transfer protein TraI OS=Sphingomonas sp. IBVSS2
 OX=1985172 GN=CAP40_12000 PE=4 SV=1
 >tr|A0A430EKX9|A0A430EKX9_9SPHN TrbI/VirB10 family protein OS=Sphingomonas sp. ABOLE
 OX=1985878 GN=CA234_07595 PE=4 SV=1
 >tr|A0A2D5HG80|A0A2D5HG80_9SPHN Conjugal transfer protein TraI OS=Novosphingobium sp.
 OX=1874826 GN=CMH85_16865 PE=4 SV=1
 >tr|T0I006|T0I006_9SPHN Conjugal transfer protein TraI OS=Sphingobium baderi LL03 OX=1114964
 GN=L485_07080 PE=4 SV=1
 >tr|A0A2A8HMY8|A0A2A8HMY8_9SPHN Conjugal transfer protein TraI OS=Novosphingobium sp. PC22D
 OX=1962403 GN=B2G71_22675 PE=4 SV=1
 >tr|A0A239IYG2|A0A239IYG2_9SPHN Type IV secretion system protein VirB10 OS=Sphingopyxis indica
 OX=436663 GN=SAMN06295955_108203 PE=4 SV=1

Protein sequence identity search was conducted using blastp at Uniprot (<https://www.uniprot.org>) in May 2019. Only amino acid identity higher than 65% and E-value=0.0 are shown. *Sphingomonas* spp. are highlighted in green.

Table S3. Metaproteomics data for bacteria identified in the midgut of both infected and uninfected ticks, Related to STAR Methods.

Accession ID	Protein description	Classification	Midgut uninfected (PSM)	Midgut infected (PSM)	Midgut infected/uninfected (PSM)
A0A067ALZ9 A8GW07 A8GY40 A0A0K6HPI9 Q0C100 A0A0Q8MPA5 A0A0P0HDM6	60 kDa chaperonin ATP synthase subunit beta	<i>Anaplasma phagocytophilum</i>	13	205	15.77*
A0A067AGK9 A8EZL8 D2XIV5 A0A067AK34 B1NAN5 C4YZR6 A0A0F3RD98 A0A0K0VLE8 A0A067AC79 A0A0F3MTX4	Adhesin Elongation factor Tu Peptidoglycan-associated protein OmpB Biotin synthase Hsp20 Small Hsp Bacterial DNA-binding family protein	<i>Rickettsia</i> spp.	25	3	0.12*
I5BVZ3	ATP synthase subunit alpha	Unidentifiable	3	13	4.33*
A0A0Q7TMJ7	ATP synthase subunit alpha	Unidentifiable	2	2	1.00
Q2YGA9	ATP synthase subunit beta	Unidentifiable	2	58	29.00*
K2JKS2	Isocitrate dehydrogenase	Unidentifiable	5	1	0.20*
A8IPT1	Chaperone protein DnaK	Unidentifiable	23	6	0.26*
A0A074K7Y6	Chaperone protein DnaK	Unidentifiable	2	3	1.50
A0A077C3L8	ATP synthase subunit alpha	Unidentifiable	1	2	2.00
Q2RXI4	Isocitrate dehydrogenase	Unidentifiable	2	1	0.50
A0A0M6YY88	ATP synthase subunit beta	Rhodobacteraceae	1	3	3.00
A0A369W0J0/ A0A0H3FY43	ATP synthase subunit b	Sphingomonadaceae	1	2	2.00